P84. Genetic Variation of Hordein Subunits in Korean Barley

Lee, S. S.*, J. W. Haam*, M. S. Lee*, J. H. Nam, K. G. Park**, H. S. Kim**, H. Y. Heo**, and Y. W. Seo*†**

*Dept. of Crop Science, College of Life and Environmental Sciences, Korea University, **National Crop Experiment Station

이성신*, 함재웅*, 이미소*, 남중현**, 박광근**, 김홍식**, 허화영**, 서용원*†

*고려대학교 식량자원학과, **작물시험장

Objectives

The purpose of this study is to develop electrophoretic system for hordein polypeptides separation and to identify hordein subunits for protein fingerprints which could be used as biochemical genetic markers for progeny analysis and plant identification in barley breeding programs.

Materials and Methods

Plant materials

Barley seed samples of 92 cultivars and experimental lines including 4 malting cultivars were provided by the National Crop Experimental Station at Suwon. Six extra-low endosperm protein barley germplasms evaluated at Aberdeen, ID, and 6 malting barley cultivars were provided by NSGRF.

Preparation of hordeins

Hordeins were extracted from 40 mg flour sample with 1 ml 55% (v/v) aqueous isopropanol containing 2% (v/v) β-mercaptoethanol at 60℃ for 30 min in a sonication bath. Hordeins were precipitated from the supernatants by the addition of an equal volume of ice-cold 1.0 M NaCl.

Hordein subunit fractionation

Hordein extracts were separated by 1D SDS-PAGE with 14% acrylamide and 0.26% bis-acrlyamide. Samples (3 $\mu\ell$ each) were loaded in the gel and subjected to electrophoresis at 20 mA. Following electrophoretic separation, gels were silver-stained.

Results and Discussion

◈ Most variable subunits were 68.0, 67.4, 64.8, and 63.6 kDa C hordeins: these subunits were present in foreign malting barley but absent in Korean malting barley cultivars. In contrast, less polymorphic hordein polypeptides were found in low protein barley germplasms than those found in Korean barley cultivars and experimental lines (Fig. 1 and 2).

◈ Korean malting barleys showed unique subunits such as 48.5, 58.9, 60.0, and 61.2 kDa bands which were not found in foreign malting barleys (Fig. 1 and 2).

◈ Analyses of hordeins from 92 barley cultivars, 6 low-protein germplasms, and 10 malting barley cultivars yielded 7 different hordein pattern groups. Fourteen components occurring in 7 hordein pattern groups were identified in Korean barley cultivars and germplasm (Fig. 3).

◈ 1D SDS-PAGE patterns of hordein polypeptides could provide useful biochemical genetic information for the identification or grouping of Korean barley cultivars and experimental lines.

서용원; Tel: 02-3290-3005, E-mail: seoag@korea.ac.kr

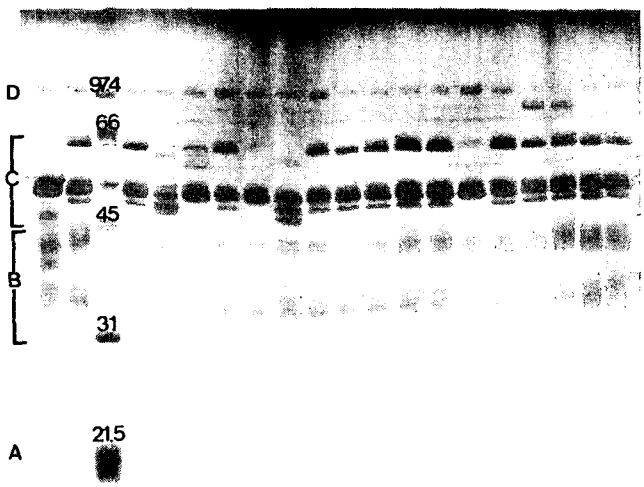

Fig. 1. Genetic variation of hordein subunits used as biochemical genetic markers. Lane 1:Suwon203, lane 2: Suwon204, lane 3: molecular size marker(kDa), lane 4: Suwon205, lane 5: Suwon206, lane 6: Suwon207, lane 8: Suwon209, lane 9: Suwon212, lane 10: Suwon214, lane 11: Suwon216, lane 12: Suwon229, lane 13: Suwon231, lane 14: Suwon232, lane 15: Suwon234, lane 16: Suwon235, lane 17: Suwon238, lane 18: Suwon239, lane 19: Suwon241, and lane 20: Suwon242. The D, C, B, and A designate the range of each hordein.

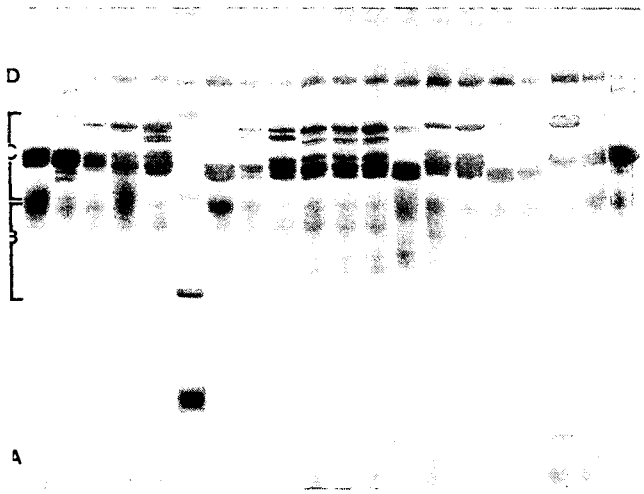

Fig. 2. Hordein subunit profiles of extra-low protein germplasms and malting barley cultivars. Lane 1: K947, lane 2: K951, lane 3: K954, lane 4: Karl, lane 5: Morex, lane 6: molecular size marker (kDa), lane 7: K970, lane 8: K973, lane 9: K974, lane 10: Robust, lane 11: Stander, lane 12: Forster, lane 13: Harrington, lane 14: Jinyangbori, lane 15: Namhyangbori, lane 16: Dusan8, lane 17: Doosan29, lane 18: Olbori, lane 19: K947, and lane 20: 951. Lane 1, 2, 3, 7, 8, and 9: extra-low protein barleys, lane 4, 5, 10, 11, 12, and 13: foreign malting barleys, lane 14, 15, 16, and 17: Korean malting barleys.

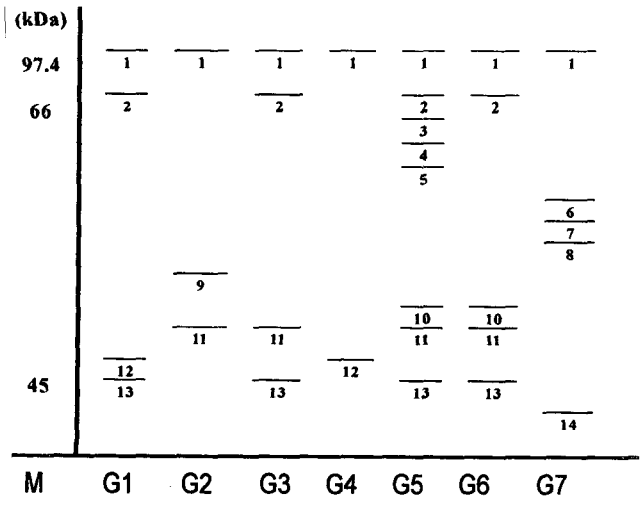

Fig. 3. Electrophoretic profiles of 7 hordein pattern groups (G: group, M: molecular size marker).